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TECH CENTER 1600/2900

#30/ff
09-19-01
1752

RAW SEQUENCE LISTING

PATENT APPLICATION: US/08/403,803A

DATE: 07/20/2001

TIME: 13:26:03

Input Set : A:\41426-A-PCT-US.txt

Output Set: N:\CRF3\07202001\H403803A.raw

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FEB 04 2002

TECH CENTER 1600/2900

Does Not Comply
Corrected Diskette Needed
See Add 1 & Add 2

3 <110> APPLICANT: Ron S. Israeli et al.
 5 <120> TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN
 7 <130> FILE REFERENCE: 1769/41426-C/JPW/SHS
 --> 9 <140> CURRENT APPLICATION NUMBER: US/08/403,803A
 --> 9 <141> CURRENT FILING DATE: 1999-10-26
 9 <160> NUMBER OF SEQ ID NOS: 38
 11 <170> SOFTWARE: PatentIn version 3.0
 13 <210> SEQ ID NO: 1
 14 <211> LENGTH: 2653
 15 <212> TYPE: DNA
 16 <213> ORGANISM: human
 18 <400> SEQUENCE: 1

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23	gcgaattcca	gcctgcagg	ctgataagcg	aggcattagt	gagattgaga	gagactttac	180
25	cccgccgtgg	tggttggagg	gcgcgcagta	gagcagcagc	acaggcgcgg	gtcccgggag	240
27	cccggtcttg	ctcgcgcgga	gatgtggaat	ctccttcacg	aaaccgactc	ggctgtggcc	300
29	accgcgcgcc	gccgcgcgtg	gctgtgcgct	ggggcgctgg	tgctggcggg	tggtctcttt	360
31	ctcctcggtc	tcctcttcgg	gtggtttata	aaatcctcca	atgaagctac	taacattact	420
33	ccaaagcata	atatgaaagc	atttttggat	gaattgaaag	ctgagaacat	caagaagttc	480
35	ttatataatt	ttacacagat	accacattta	gcaggaaacg	aacaaaactt	tcagcttgca	540
37	aagcaaattc	aatcccagtg	gaaagaattt	ggcctggatt	ctggttgagc	agcacattat	600
39	gatgtcctgt	tgctctaccc	aaataagact	catcccaact	acatctcaat	aattaatgaa	660
41	gatggaaatg	agattttcaa	cacatcatta	tttgaaccac	ctcctccagg	atatgaaaat	720
43	gtttcggata	ttgtaccacc	tttcagtgct	ttctctcctc	aaggaaatgcc	agagggcgat	780
45	ctagtgtatg	ttaactatgc	acgaactgaa	gacttcttta	aattggaacg	ggacatgaaa	840
47	atcaattgct	ctgggaaaat	tgtaattgcc	agatatggga	aagttttcag	aggaaataag	900
49	gttaaaaaatg	cccagctggc	aggggccaaa	ggagtcattc	tctactccga	ccctgtctgac	960
51	tactttgtctc	ctggggtgaa	gtcctatcca	gatggttgga	atcttctctg	aggtggtgtc	1020
53	cagcgtggaa	atatacctaaa	tctgaatggg	gcaggagacc	ctctcacacc	aggttaccca	1080
55	gcaaatgaat	atgcttatag	gcgtggaatt	gcagaggtct	ttggtcttcc	aagtattcct	1140
57	gttcatocaa	ttggatacta	tgatgcacag	aagctcctag	aaaaaatggg	tggtcagca	1200
59	ccaccagata	gcagctggag	aggaaagtctc	aaagtgcctc	acaatgttgg	acctggcttt	1260
61	actggaaaact	ttctacaca	aaaagtcaag	atgcacatcc	actctaccaa	tgaagtgaca	1320
63	agaatttaca	atgtgatagg	tactctcaga	ggagcagtg	aaccagacag	atatgtcatt	1380
65	ctgggaggtc	accgggactc	atgggtgttt	ggtggtattg	accctcagag	tgagcagct	1440
67	gttggtcatg	aaattgtgag	gagctttgga	acactgaaaa	aggaagggtg	gagacctaga	1500
69	agaacaattt	tgtttgcaag	ctgggatgca	gaagaatttg	gtcttcttgg	ttctactgag	1560
71	tgggcagagg	agaattcaag	actccttcaa	gagcgtggcg	tggttatat	taatgctgac	1620
73	tcactctatg	aaggaaacta	cactctgaga	gttgattgta	caccgctgat	gtacagcttg	1680
75	gtacacaacc	taacaaaaga	gctgaaaagc	cctgatgaag	gctttgaagg	caaatctctt	1740
77	tatgaaagtt	ggactaaaaa	aagtccttcc	ccagagttca	gtggcatgcc	caggataagc	1800
79	aaattgggat	ctggaaatga	ttttgaggtg	ttcttccaac	gacttggaat	tgcttcaggc	1860
81	agagcacggt	atactaaaaa	ttgggaaaca	aacaaattca	gcccgtatcc	actgtatcac	1920
83	agtgtctatg	aaacatatga	gttgggtggaa	aagttttatg	atccaatgtt	taaatatcac	1980
85	ctcactgtgg	cccaggttcg	aggaggatg	gtgtttgagc	tagccaattc	catagtgtctc	2040
87	ccttttgatt	gtcgaagatt	tgctgtagtt	ttaagaaagt	atgctgacaa	aatctacagt	2100

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Input Set : A:\41426-A-PCT-US.txt

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```

89 atttctatga aacatccaca ggaaatgaag acatacagtg tatcatttga ttcacttttt 2160
91 totgcagtaa agaattttac agaaattgct tccaagttca gtgagagact ccaggactft 2220
93 gacaaaagca acccaatagt attaagaatg atgaatgac aactcatgtt tctggaaaga 2280
95 gcattttattg atccattagg gttaccagac aggccttttt ataggcatgt catctatgct 2340
97 ccaagcagcc acaacaagta tgcaggggag tcattcccag gaatttatga tgctctgttt 2400
99 gatattgaaa gcaagtgga cccttccaag gcctggggag aagtgaagag acagatttat 2460
101 gttgcagcct tcacagtgc ggcagctgca gagactttga gtgaagtagc ctaagaggat 2520
103 tcttttagaga atccgtattg aatttgtgtg gtatgtcact cagaaagaat cgtaatgggt 2580
105 atattgataa attttaaaat tggatatatt gaaataaagt tgaatattat atataaaaaa 2640
107 aaaaaaaaaa aaa 2653
110 <210> SEQ ID NO: 2
111 <211> LENGTH: 750
112 <212> TYPE: PRT
113 <213> ORGANISM: human
115 <400> SEQUENCE: 2
117 Met Trp Asn Leu Leu His Glu Thr Asp Ser Ala Val Ala Thr Ala Arg
118 1 5 10 15
120 Arg Pro Arg Trp Leu Cys Ala Gly Ala Leu Val Leu Ala Gly Gly Phe
121 20 25 30
123 Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe Ile Lys Ser Ser Asn Glu
124 35 40 45
126 Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala Phe Leu Asp Glu
127 50 55 60
129 Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu Tyr Asn Phe Thr Gln Ile
130 65 70 75 80
132 Pro His Leu Ala Gly Thr Glu Gln Asn Phe Gln Leu Ala Lys Gln Ile
133 85 90 95
135 Gln Ser Gln Trp Lys Glu Phe Gly Leu Asp Ser Val Glu Leu Ala His
136 100 105 110
138 Tyr Asp Val Leu Leu Ser Tyr Pro Asn Lys Thr His Pro Asn Tyr Ile
139 115 120 125
141 Ser Ile Ile Asn Glu Asp Gly Asn Glu Ile Phe Asn Thr Ser Leu-Phe
142 130 135 140
144 Glu Pro Pro Pro Pro Gly Tyr Glu Asn Val Ser Asp Ile Val Pro Pro
145 145 150 155 160
147 Phe Ser Ala Phe Ser Pro Gln Gly Met Pro Glu Gly Asp Leu Val Tyr
148 165 170 175
150 Val Asn Tyr Ala Arg Thr Glu Asp Phe Phe Lys Leu Glu Arg Asp Met
151 180 185 190
153 Lys Ile Asn Cys Ser Gly Lys Ile Val Ile Ala Arg Tyr Gly Lys Val
154 195 200 205
156 Phe Arg Gly Asn Lys Val Lys Asn Ala Gln Leu Ala Gly Ala Lys Gly
157 210 215 220
159 Val Ile Leu Tyr Ser Asp Pro Ala Asp Tyr Phe Ala Pro Gly Val Lys
160 225 230 235 240
162 Ser Tyr Pro Asp Gly Trp Asn Leu Pro Gly Gly Gly Val Gln Arg Gly
163 245 250 255
165 Asn Ile Leu Asn Leu Asn Gly Ala Gly Asp Pro Leu Thr Pro Gly Tyr
166 260 265 270

```

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```

168 Pro Ala Asn Glu Tyr Ala Tyr Arg Arg Gly Ile Ala Glu Ala Val Gly
169           275           280           285
171 Leu Pro Ser Ile Pro Val His Pro Ile Gly Tyr Tyr Asp Ala Gln Lys
172           290           295           300
174 Leu Leu Glu Lys Met Gly Gly Ser Ala Pro Pro Asp Ser Ser Trp Arg
175 305           310           315           320
177 Gly Ser Leu Lys Val Pro Tyr Asn Val Gly Pro Gly Phe Thr Gly Asn
178           325           330           335
180 Phe Ser Thr Gln Lys Val Lys Met His Ile His Ser Thr Asn Glu Val
181           340           345           350
183 Thr Arg Ile Tyr Asn Val Ile Gly Thr Leu Arg Gly Ala Val Glu Pro
184           355           360           365
186 Asp Arg Tyr Val Ile Leu Gly Gly His Arg Asp Ser Trp Val Phe Gly
187           370           375           380
189 Gly Ile Asp Pro Gln Ser Gly Ala Ala Val Val His Glu Ile Val Arg
190 385           390           395           400
192 Ser Phe Gly Thr Leu Lys Lys Glu Gly Trp Arg Pro Arg Arg Thr Ile
193           405           410           415
195 Leu Phe Ala Ser Trp Asp Ala Glu Glu Phe Gly Leu Leu Gly Ser Thr
196           420           425           430
198 Glu Trp Ala Glu Glu Asn Ser Arg Leu Leu Gln Glu Arg Gly Val Ala
199           435           440           445
201 Tyr Ile Asn Ala Asp Ser Ser Ile Glu Gly Asn Tyr Thr Leu Arg Val
202           450           455           460
204 Asp Cys Thr Pro Leu Met Tyr Ser Leu Val His Asn Leu Thr Lys Glu
205 465           470           475           480
207 Leu Lys Ser Pro Asp Glu Gly Phe Glu Gly Lys Ser Leu Tyr Glu Ser
208           485           490           495
210 Trp Thr Lys Lys Ser Pro Ser Pro Glu Phe Ser Gly Met Pro Arg Ile
211           500           505           510
213 Ser Lys Leu Gly Ser Gly Asn Asp Phe Glu Val Phe Phe Gln Arg Leu
214           515           520           525
216 Lys Ile Ala Ser Gly Arg Ala Arg Tyr Thr Lys Asn Trp Glu Thr Asn
217           530           535           540
219 Lys Phe Ser Gly Tyr Pro Leu Tyr His Ser Val Tyr Glu Thr Tyr Glu
220 545           550           555           560
222 Leu Val Glu Lys Phe Tyr Asp Pro Met Phe Lys Tyr His Leu Thr Val
223           565           570           575
225 Ala Gln Val Arg Gly Gly Met Val Phe Glu Leu Ala Asn Ser Ile Val
226           580           585           590
228 Leu Pro Phe Asp Cys Arg Asp Tyr Ala Val Val Leu Arg Lys Tyr Ala
229           595           600           605
231 Asp Lys Ile Tyr Ser Ile Ser Met Lys His Pro Gln Glu Met Lys Thr
232           610           615           620
234 Tyr Ser Val Ser Phe Asp Ser Leu Phe Ser Ala Val Lys Asn Phe Thr
235 625           630           635           640
237 Glu Ile Ala Ser Lys Phe Ser Glu Arg Leu Gln Asp Phe Asp Lys Ser
238           645           650           655
240 Asn Pro Ile Val Leu Arg Met Met Asn Asp Gln Leu Met Phe Leu Glu

```

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```

241          660          665          670
243 Arg Ala Phe Ile Asp Pro Leu Gly Leu Pro Asp Arg Pro Phe Tyr Arg
244          675          680          685
246 His Val Ile Tyr Ala Pro Ser Ser His Asn Lys Tyr Ala Gly Glu Ser
247          690          695          700
249 Phe Pro Gly Ile Tyr Asp Ala Leu Phe Asp Ile Glu Ser Lys Val Asp
250 705          710          715          720
252 Pro Ser Lys Ala Trp Gly Glu Val Lys Arg Gln Ile Tyr Val Ala Ala
253          725          730          735
255 Phe Thr Val Gln Ala Ala Ala Glu Thr Leu Ser Glu Val Ala
256          740          745          750
258 <210> SEQ ID NO: 3
259 <211> LENGTH: 8
260 <212> TYPE: PRT
261 <213> ORGANISM: human
263 <400> SEQUENCE: 3
265 Ser Leu Tyr Glu Ser Trp Thr Lys
266 1          5
268 <210> SEQ ID NO: 4
269 <211> LENGTH: 15
270 <212> TYPE: PRT
271 <213> ORGANISM: human
273 <220> FEATURE:
--> 274 <221> NAME/KEY: misc.
275 <222> LOCATION: (1)..(15)
276 <223> OTHER INFORMATION: x=unknown
279 <400> SEQUENCE: 4
--> 281 Ser Tyr Pro Asp Gly Xaa Xaa Leu Pro Gly Gly Gly Val Gln Arg
282 1          5          10          15
284 <210> SEQ ID NO: 5
285 <211> LENGTH: 7
286 <212> TYPE: PRT
287 <213> ORGANISM: human
289 <400> SEQUENCE: 5
291 Phe Tyr Asp Pro Met Phe Lys
292 1          5
294 <210> SEQ ID NO: 6
295 <211> LENGTH: 9
296 <212> TYPE: PRT
297 <213> ORGANISM: human
299 <400> SEQUENCE: 6
301 Ile Tyr Asn Val Ile Gly Thr Leu Lys
302 1          5
304 <210> SEQ ID NO: 7
305 <211> LENGTH: 22
306 <212> TYPE: PRT
307 <213> ORGANISM: human
309 <220> FEATURE:
--> 310 <221> NAME/KEY: misc

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```

311 <222> LOCATION: (1)..(22)
312 <223> OTHER INFORMATION: x=unknown
315 <400> SEQUENCE: 7
-> 317 Phe Leu Tyr Xaa Xaa Thr Gln Ile Pro His Leu Ala Gly Thr Glu Gln
318 1 5 10 15
320 Asn Phe Gln Leu Ala Lys
321 20
323 <210> SEQ ID NO: 8
324 <211> LENGTH: 17
325 <212> TYPE: PRT
326 <213> ORGANISM: human
328 <400> SEQUENCE: 8
330 Gly Val Ile Leu Tyr Ser Asp Pro Ala Asp Tyr Phe Ala Pro Asp Val
331 1 5 10 15
333 Lys
336 <210> SEQ ID NO: 9
337 <211> LENGTH: 17
338 <212> TYPE: PRT
339 <213> ORGANISM: human
341 <400> SEQUENCE: 9
343 Pro Val Ile Leu Tyr Ser Asp Pro Ala Asp Tyr Phe Ala Pro Gly Val
344 1 5 10 15
346 Lys
349 <210> SEQ ID NO: 10
350 <211> LENGTH: 15
351 <212> TYPE: PRT
352 <213> ORGANISM: human
354 <400> SEQUENCE: 10
356 Ala Phe Ile Asp Pro Leu Gly Leu Pro Asp Arg Pro Phe Tyr Arg
357 1 5 10 15
359 <210> SEQ ID NO: 11
360 <211> LENGTH: 19
361 <212> TYPE: PRT
362 <213> ORGANISM: human
364 <400> SEQUENCE: 11
366 Tyr Ala Gly Glu Ser Phe Pro Gly Ile Tyr Asp Ala Leu Phe Asp Ile
367 1 5 10 15
369 Glu Ser Lys
372 <210> SEQ ID NO: 12
373 <211> LENGTH: 22
374 <212> TYPE: PRT
375 <213> ORGANISM: human
377 <220> FEATURE:
--> 378 <221> NAME/KEY: misc.
379 <222> LOCATION: (1)..(22)
380 <223> OTHER INFORMATION: x=unknown
383 <400> SEQUENCE: 12
--> 385 Thr Ile Leu Phe Ala Ser Trp Asp Ala Glu Glu Phe Gly Xaa Xaa Gly
386 1 5 10 15

```

Use of 'n' and/or 'Xaa' has been detected in the Sequence Listing. Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using 'n' or 'Xaa'.

● Add 1

<210> 13

<211> 17

<212> DNA

<213> artificial;primer

<220>

<221> misc.

<222> (1)..(16)

<223> n=unknown

<400> 13

ttytaygayc cnatgtt

17

<210> 14

<211> 17

<212> DNA

<213> artificial;primer

<220>

<221> misc

<222> (1)..(16)

<223> n=unknown

<400> 14

aacatnggrt crtaraa

17

<210> 15

<211> 17

<212> DNA

<213> artificial;primer

<220>

<221> misc.

see item # 10 on
ERROR summary
SHEET
↓↓

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

● Add 2

<210> 30

<211> 27

<212> DNA

<213> artificial

— see item # 11 on ERROR
Summary SHEET.

<400> 30

acggagcaaa acttcagct tgcaaag

27

VERIFICATION SUMMARY

PATENT APPLICATION: US/08/403,803A

DATE: 07/20/2001

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Input Set : A:\41426-A-PCT-US.txt

Output Set: N:\CRF3\07202001\H403803A.raw

9 M:270 C: Current Application Number differs, Replaced Current Application No
9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
274 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
281 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
310 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
317 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
378 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:12
385 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
394 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13
397 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13
403 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
409 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14
412 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14
418 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
424 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15
427 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15
433 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
439 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16
442 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:16
448 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
454 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:17
457 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:17
463 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
469 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:18
472 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:18
478 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
484 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:19
487 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:19
493 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
499 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:20
502 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20
508 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
514 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:21
516 M:258 W: Mandatory Feature missing, <220> FEATURE:
516 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
523 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:22
525 M:258 W: Mandatory Feature missing, <220> FEATURE:
525 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
532 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:23
535 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:23
541 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
547 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:24
550 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:24
556 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
562 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:25
565 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
571 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
577 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:26

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580 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
586 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
595 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
603 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
607 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
609 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
619 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
621 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
625 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
634 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:28
646 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
648 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
652 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
654 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
656 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
658 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
669 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:29
681 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
687 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
697 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:30
699 M:258 W: Mandatory Feature missing, <220> FEATURE:
699 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
706 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:31
708 M:258 W: Mandatory Feature missing, <220> FEATURE:
708 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
716 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:32
718 M:258 W: Mandatory Feature missing, <220> FEATURE:
718 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
725 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:33
727 M:258 W: Mandatory Feature missing, <220> FEATURE:
727 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
734 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:34
736 M:258 W: Mandatory Feature missing, <220> FEATURE:
736 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:

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SEP 11 2001

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Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 08/403,803A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) 30 missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

Attachment for PTO-948 (Rev. 03/01, or earlier)

6/18/01

The below text replaces the pre-printed text under the heading, "Information on How to Effect Drawing Changes," on the back of the PTO-948 (Rev. 03/01, or earlier) form.

INFORMATION ON HOW TO EFFECT DRAWING CHANGES

1. Correction of Informalities -- 37 CFR 1.85

New corrected drawings must be filed with the changes incorporated therein. Identifying indicia, if provided, should include the title of the invention, inventor's name, and application number, or docket number (if any) if an application number has not been assigned to the application. If this information is provided, it must be placed on the front of each sheet and centered within the top margin. If corrected drawings are required in a Notice of Allowability (PTOL-37), the new drawings **MUST** be filed within the **THREE MONTH** shortened statutory period set for reply in the Notice of Allowability. Extensions of time may **NOT** be obtained under the provisions of 37 CFR 1.136(a) or (b) for filing the corrected drawings after the mailing of a Notice of Allowability. The drawings should be filed as a separate paper with a transmittal letter addressed to the Official Draftsperson.

2. Corrections other than Informalities Noted by Draftsperson on form PTO-948.

All changes to the drawings, other than informalities noted by the Draftsperson, **MUST** be made in the same manner as above except that, normally, a highlighted (preferably red ink) sketch of the changes to be incorporated into the new drawings **MUST** be approved by the examiner before the application will be allowed. No changes will be permitted to be made, other than correction of informalities, unless the examiner has approved the proposed changes.

Timing of Corrections

Applicant is required to submit the drawing corrections within the time period set in the attached Office communication. See 37 CFR 1.85(a).

Failure to take corrective action within the set period will result in **ABANDONMENT** of the application.

06/01/01